Package ‘tanggle’

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Type Package

Title Visualization of Phylogenetic Networks

Version 1.11.0

Description Offers functions for plotting split (or implicit) networks (unrooted, undirected) and explicit networks (rooted, directed) with reticulations extending. 'ggtree' and using functions from 'ape' and 'phangorn'. It extends the 'ggtree' package [@Yu2017] to allow the visualization of phylogenetic networks using the 'ggplot2' syntax. It offers an alternative to the plot functions already available in 'ape' Paradis and Schliep (2019) <doi:10.1093/bioinformatics/bty633> and 'phangorn' Schliep (2011) <doi:10.1093/bioinformatics/btq706>.

Depends R (>= 4.1), ggplot2 (>= 2.2.0), ggtree

Imports ape (>= 5.0), phangorn (>= 2.5), utils, methods

Suggests tinytest, BiocStyle, ggimage, knitr, rmarkdown

VignetteBuilder knitr

biocViews Software, Visualization, Phylogenetics, Alignment, Clustering, MultipleSequenceAlignment, DataImport

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URL https://klausvigo.github.io/tanggle, https://github.com/KlausVigo/tanggle

BugReports https://github.com/KlausVigo/tanggle/issues

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Roxygen list(old_usage = TRUE)

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Contents

`tanggle-package` *tanggle: Visualization of Phylogenetic Networks*

Description

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See Also

Useful links:

- https://klausvigo.github.io/tanggle
- https://github.com/KlausVigo/tanggle
- Report bugs at https://github.com/KlausVigo/tanggle/issues

geom_splitnet *geom_splitnet*

Description

add splitnet layer

Usage

```
geom_splitnet(layout = "slanted", ...)
```

Arguments

layout	one of 'rectangular', 'slanted', 'circular', 'radial' or 'unrooted'
...	additional parameter

Value

splitnet layer

Author(s)

Klaus Schliep

Examples

```
data(yeast, package='phangorn')
dm <- phangorn::dist.ml(yeast)
nnet <- phangorn::neighborNet(dm)
ggplot(nnet, aes(x, y))  + geom_splitnet() + theme_tree()
```

ggevonet *ggevonet*

Description

drawing phylogenetic tree from phylo object

Usage

```
ggevonet(tr, mapping = NULL, layout = "slanted", mrsd = NULL,
  as.Date = FALSE, yscale = "none", yscale_mapping = NULL,
  ladderize = FALSE, right = FALSE, branch.length = "branch.length",
  ndigits = NULL, min_crossing = TRUE, ...)
```

Arguments

tr	a evonet object
mapping	aes mapping
layout	one of 'rectangular', 'slanted'
mrsd	most recent sampling date
as.Date	logical whether using Date class in time tree
yscale	y scale
yscale_mapping	yscale mapping for category variable
ladderize	logical
right	logical
branch.length	variable for scaling branch, if 'none' draw cladogram
ndigits	number of digits to round numerical annotation variable
min_crossing	logical, rotate clades to minimize crossings
...	additional parameter

Value

tree

Author(s)

Klaus Schliep

See Also

evonet, ggtree

Examples

```
(enet <- ape::read.evonet(text='((a:2,(b:1)#H1:1):1,(#H1,c:1):2);'))
ggevonet(enet) + geom_tiplab()
```

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ggsplitnet *ggsplitnet*

Description

drawing phylogenetic tree from phylo object

Usage

```
ggsplitnet(tr, mapping = NULL, layout = "slanted", mrsd = NULL,
  as.Date = FALSE, yscale = "none", yscale_mapping = NULL,
  ladderize = FALSE, right = FALSE, branch.length = "branch.length",
  ndigits = NULL, ...)
```

Arguments

`tr`	a networx object
`mapping`	aes mapping
`layout`	so far only 'slanted' is supported.
`mrsd`	most recent sampling date
`as.Date`	logical whether using Date class in time tree
`yscale`	y scale
`yscale_mapping`	yscale mapping for category variable
`ladderize`	logical
`right`	logical
`branch.length`	variable for scaling branch, if 'none' draw cladogram
`ndigits`	number of digits to round numerical annotation variable
`...`	additional parameter

Value

tree

Author(s)

Klaus Schliep

References

Schliep, K., Potts, A. J., Morrison, D. A. and Grimm, G. W. (2017), Intertwining phylogenetic trees and networks. *Methods Ecol Evol*. **8**, 1212–1220. doi:10.1111/2041-210X.12760

See Also

`ggtree`, `networx`, `consensusNet`, `neighborNet`

Examples

```
data(yeast, package='phangorn')
dm <- phangorn::dist.ml(yeast)
nnet <- phangorn::neighborNet(dm)
ggsplitnet(nnet) + geom_tiplab2()
```

`minimize_overlap` *minimize_overlap reduces reticulation lines crossing over in plots*

Description

minimize_overlap reduces reticulation lines crossing over in plots

Usage

```
minimize_overlap(x)
```

Arguments

x	Tree of class 'evonet'

Value

A Tree with rotated nodes of class 'evonet'

Author(s)

L. Francisco Henao Diaz

Examples

```
fishnet <- ape::read.evonet(text='(Xalvarezi,Xmayae,((Xsignum,((Xmonticolus,
(Xclemenciae_F2,#H25)),(((((((((Xgordoni,Xmeyeri),Xcouchianus),Xvariatus),
Xevelynae),(Xxiphidium,#H24)),Xmilleri),Xandersi),Xmaculatus),(((Xmontezumae,
(Xcortezi,(Xbirchmanni_GARC,Xmalinche_CHIC2))),((Xnigrensis,Xmultilineatus),
(Xpygmaeus,Xcontinens))))#H24))),(Xhellerii)#H25));')
fishnet$edge.length <- NULL
new_tre <- minimize_overlap(fishnet)

par(mfrow=c(1,2))
ggevonet(fishnet, min_crossing = FALSE)
ggevonet(new_tre)

net2 <- ape::read.evonet(text='(15,(1,((14,(#H1,(((12,13),(11,#H3)),(7,
    ((10)#H3,(8,9))))))),((((2,3))#H2,(6,(5,(#H2,4)))))#H1)));')
# Cui et al. 2013 Evol.
new_net2 <- minimize_overlap(net2)
ggevonet(net2, min_crossing = FALSE)
ggevonet(new_net2)
```

node_depth_evonet *Depth of Nodes*

Description

These functions return the depths or heights of nodes and tips.

Usage

```
node_depth_evonet(x, ...)
```

Arguments

x	an object of class 'evonet'
...	Further arguments passed to or from other methods.

Value

a vector with the depth of the nodes

See Also

node.depth

Examples

```
z <- ape::read.evonet(text = '((1,((2,(3,(4)Y#H1)g)e,
(((Y#H1, 5)h,6)f)X#H2)c)a,((X#H2,7)d,8)b)r;')
nd <- node_depth_evonet(z)
z$edge.length <- nd[z$edge[,1]] - nd[z$edge[,2]]
ggevonet(z)
```

Index